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## Claims:

- 1. A prokaryotic cell that is genetically modified to shift the redox status of the cytoplasm to a more oxidative state, and which further contains a gene encoding a catalyst of disulfide bond formation and/or isomerization.
- 5 2. The prokaryotic cell of claim 1, wherein the expression or activity of a reductase is decreased relative to that in the corresponding wild type cell.
  - 3. The prokaryotic cell of claim 2, wherein the reductase is selected from the group consisting of thioredoxin reductase, glutathione reductase, and glutathione.
- 4. The prokaryotic cell of claim 3, in which the expression or activity of a second reductase is decreased relative to that in the corresponding wild type cell.
  - 5. The prokaryotic cell of claim 4, wherein the second reductase is selected from the group consisting of thioredoxin reductase, glutathione reductase, and glutathione.
  - 6. The prokaryotic cell of claim 2, wherein the gene encoding the reductase is mutated.
  - 7. The prokaryotic cell of claim 6, wherein the gene encoding the reductase contains a null mutation.
  - 8. The prokaryotic cell of claim 5, wherein the genes encoding the first and the second reductases contain a null mutation.
  - 9. The prokaryotic cell of claim 2, wherein the activity of the reductase is inhibited.
  - 10. The prokaryotic cell of claim 9, wherein the activity of the reductase is inhibited by contacting the prokaryotic cell with an agent.
  - 11. The prokaryotic cell of claim 1, further modified to increase its ability to proliferate.
  - 12. The prokaryotic cell of claim 4, further modified to increase its ability to proliferate.
  - 13. The prokaryotic cell of claim 11, wherein the modification consists of the introduction of a suppressor mutation.
- 25 14. The prokaryotic cell of claim 12, wherein the modification consists of the introduction of a suppressor mutation.
  - 15. The prokaryotic cell of claim 11, wherein the modification restores at least some of the reducing capacity to the cytoplasm of the prokaryotic cell.
- 16. The prokaryotic cell of claim 11, wherein the modification is a mutation in the *ahpC* gene which reduces its peroxidase activity.
  - 17. The prokaryotic cell of claim 16, wherein the mutation is located in a region containing four triplet repeats.
  - 18. The prokaryotic cell of claim 17, wherein the mutated ahpC protein has the amino acid sequence set forth in SEQ ID NO: 24.
- 35 19. The prokaryotic cell of claim 1, having ATCC Designation No. PTA-938 (FA112).

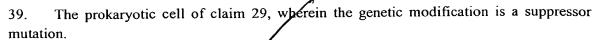
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- 20. The prokaryotic cell of claim 1, having ATCC Designation No. PTA-939 (FA113).
- 21. The prokaryotic cell of claim 19, further comprising a nucleic acid encoding a catalyst of disulfide bond formation or isomerization.
- 22. The prokaryotic cell of claim 20, further comprising a nucleic acid encoding a catalyst of disulfide bond formation or isomerization.
  - 23. A prokaryotic cell of claim 1, further comprising a heterologous nucleic acid.
  - 24. The prokaryotic cell of claim 1, which comprises a nucleic acid encoding a catalyst of disulfide bond isomerization.
  - 25. The prokaryotic cell of claim 24, which comprises a nucleic acid encoding a catalyst of disulfide bond isomerization.
  - 26. The prokaryotic cell of claim 25, wherein the catalyst is a DsbC protein or an analog thereof.
  - 27. The prokaryotic cell of claim 1, wherein the catalyst is a variant of a protein of the thioredoxin superfamily having a redox potential that is higher than that of its wild type counterpart.
  - 28. The prokaryotic cell of claim 27, wherein the variant is a "Grx" variant of thioredoxin A.
  - 29. A prokaryotic cell that is genetically modified to shift the redox status of the cytoplasm to a more oxidative, and which further contains a genetic modification to increase its ability to proliferate.
  - 30. The prokaryotic cell of claim 29, in which the expression or activity of a reductase is decreased relative to that in the corresponding wild type cell.
  - 31. The prokaryotic cell of claim 30, wherein the reductase is selected from the group consisting of thioredoxin reductase, glutathione reductase, and glutathione.
- 25 32. The prokaryotic cell of claim 30, in which the expression or activity of a second reductase is decreased relative to that in the corresponding wild type cell.
  - 33. The prokaryotic cell of claim 29, wherein the second reductase is selected from the group consisting of thioredoxin reductase, glutathione reductase, and glutathione.
  - 34. The prokaryotic cell of claim 30, wherein the gene encoding the reductase is mutated.
- 30 35. The prokaryotic cell of claim 34, wherein the gene encoding the reductase contains a null mutation.
  - 36. The prokaryotic cell of claim 32, wherein the genes encoding the first and the second reductases contain a null mutation.
  - 37. The prokaryotic cell of claim 30, wherein the activity of the reductase is inhibited.
- 35 38. The prokaryotic cell of claim 37, wherein the activity of the reductase is inhibited by contacting the prokaryotic cell with an agent.

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- 40. The prokaryotic cell of claim 29, wherein the modification restores at least some of the reducing capacity to the cytoplasm of the prokaryotic cell.
- The prokaryotic cell of claim 40, wherein the modification is a mutation in the ahpC gene which reduces its peroxidase activity.
  - 42. The prokaryotic cell of claim 41, wherein the mutation is located in a region containing four triplet repeats.
  - 43. The prokaryotic cell of claim 42, wherein the mutated ahpC protein has the amino acid sequence set forth in SEQ ID NO: 24.
- 44. The prokaryotic cell of claim 29, further containing a gene encoding a catalyst of disulfide bond formation and/or isomerization.
  - 45. The prokaryotic cell of claim 44, wherein the catalyst is a DsbC protein-
  - 46. The prokaryotic cell of claim 44, wherein the catalyst is a variant of a protein of the thioredoxin superfamily having a redox potential that is higher than that of its wild type counterpart.
  - 47. The prokaryotic cell of claim 46, wherein the variant is a "Grx" variant of thioredoxin A.
  - 48. The prokaryotic cell of claim 44, wherein expression of the gene encoding the catalyst is inducible.
  - 49. A method for producing a protein having at least one disulfide bond, comprising growing a host cell of claim 1 comprising a nucleic acid encoding a protein having at least one disulfide bond, under conditions in which the protein is produced, and isolating the protein from the host cell.
  - 50. A method for producing a protein having at least one disulfide bond, growing a host cell of claim 29 comprising a nucleic acid encoding a protein having at least one disulfide bond, under conditions in which the protein is produced, and isolating the protein from the host cell.
  - 51. A protein produced by the method of claim 49.
- 30 52. A protein produced by the method of claim 50.
  - 53. Tissue plasminogen activator (PA) produced by the method of claim 49.
  - 54. Tissue plasminogen activator (tPA) produced by the method of claim 50.

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